

05/20
10/11

OIPE

#3

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/676,436

DATE: 11/07/2001

TIME: 15:14:33

Input Set : A:\RTS-0169_Seq_ASCII.txt
 Output Set: N:\CRF3\11072001\I676436.raw

3 <110> APPLICANT: Donna T. Ward
 4 William Gaarde
 5 Brett P. Monia
 6 Jacqueline Wyatt
 8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK4 EXPRESSION
 10 <130> FILE REFERENCE: RTS-0169
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/676,436
 C--> 12 <141> CURRENT FILING DATE: 2000-09-29
 12 <160> NUMBER OF SEQ ID NOS: 89
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 20
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Artificial Sequence ✓
 W--> 20 <220> FEATURE:
 20 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓
 22 <400> SEQUENCE: 1
 23 tccgtcatcg ctcctcaggg ✓
 26 <210> SEQ ID NO: 2
 27 <211> LENGTH: 20
 28 <212> TYPE: DNA ✓
 29 <213> ORGANISM: Artificial Sequence ✓
 W--> 31 <220> FEATURE:
 31 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓
 33 <400> SEQUENCE: 2
 34 atgcattctg cccccaagga ✓
 37 <210> SEQ ID NO: 3
 38 <211> LENGTH: 4990
 39 <212> TYPE: DNA ✓
 40 <213> ORGANISM: Homo sapiens
 42 <220> FEATURE:
 43 <221> NAME/KEY: CDS
 44 <222> LOCATION: (1)...(4476)
 46 <400> SEQUENCE: 3
 47 cta gaa gac ttc tcc gat gaa aca aat aca gag aat ctt tat ggt acc 48
 48 Leu Glu Asp Phe Ser Asp Glu Thr Asn Thr Glu Asn Leu Tyr Gly Thr
 49 1 5 10 15
 51 tct ccc ccc agc aca cct cga cag atg aaa cgc atg tca acc aaa cat 96
 52 Ser Pro Pro Ser Thr Pro Arg Gln Met Lys Arg Met Ser Thr Lys His
 53 20 25 30
 55 cag agg aat aat gtg ggg agg cca gcc agt cgg tct aat ttg aaa gaa 144
 56 Gln Arg Asn Asn Val Gly Arg Pro Ala Ser Arg Ser Asn Leu Lys Glu
 57 35 40 45
 59 aaa atg aat gca cca aat cag cct cca cat aaa gac act gga aaa aca 192
 60 Lys Met Asn Ala Pro Asn Gln Pro Pro His Lys Asp Thr Gly Lys Thr
 61 50 55 60
 63 gtg gag aat gtg gaa gaa tac agc tat aag cag gag aaa aag atc cga 240
 64 Val Glu Asn Val Glu Glu Tyr Ser Tyr Lys Gln Glu Lys Lys Ile Arg

ENTERED

20
ENTERED

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65	65	70	75	80													
67	gca	gct	ctt	aga	aca	aca	gag	cgt	gat	cat	aaa	aaa	aat	gta	cag	tgc	288
68	Ala	Ala	Leu	Arg	Thr	Thr	Glu	Arg	Asp	His	Lys	Lys	Asn	Val	Gln	Cys	
69																95	
71	tca	ttc	atg	tta	gac	tca	gtg	ggt	gga	tct	ttg	cca	aaa	aaa	tca	att	336
72	Ser	Phe	Met	Leu	Asp	Ser	Val	Gly	Gly	Ser	Leu	Pro	Lys	Lys	Ser	Ile	
73																110	
75	cca	gat	gtg	gat	ctc	aat	aag	cct	tac	ctc	agc	ctt	ggc	tgt	agc	aat	384
76	Pro	Asp	Val	Asp	Leu	Asn	Lys	Pro	Tyr	Leu	Ser	Leu	Gly	Cys	Ser	Asn	
77																125	
79	gct	aag	ctt	cca	gta	tct	gtg	ccc	atg	cct	ata	gcc	aga	cct	gca	cgc	432
80	Ala	Lys	Leu	Pro	Val	Ser	Val	Pro	Met	Pro	Ile	Ala	Arg	Pro	Ala	Arg	
81																140	
83	cag	act	tct	agg	act	gac	tgt	cca	gca	gat	cgt	tta	aag	ttt	ttt	gaa	480
84	Gln	Thr	Ser	Arg	Thr	Asp	Cys	Pro	Ala	Asp	Arg	Leu	Lys	Phe	Phe	Glu	
85	145															160	
87	act	tta	cga	ctt	ttg	cta	aag	ctt	acc	tca	gtc	tca	aag	aaa	aaa	gac	528
88	Thr	Leu	Arg	Leu	Leu	Leu	Lys	Leu	Thr	Ser	Val	Ser	Lys	Lys	Lys	Asp	
89																175	
91	agg	gag	caa	aga	gga	caa	gaa	aat	acg	tct	ggt	ttc	tgg	ctt	aac	cga	576
92	Arg	Glu	Gln	Arg	Gly	Gln	Glu	Asn	Thr	Ser	Gly	Phe	Trp	Leu	Asn	Arg	
93																190	
95	tct	aac	gaa	ctg	atc	tgg	tta	gag	cta	caa	gcc	tgg	cat	gca	gga	cgg	624
96	Ser	Asn	Glu	Leu	Ile	Trp	Leu	Glu	Leu	Gln	Ala	Trp	His	Ala	Gly	Arg	
97																205	
99	aca	att	aac	gac	cag	gac	ttc	ttt	tta	tat	aca	gcc	cgt	caa	gcc	atc	672
100	Thr	Ile	Asn	Asp	Gln	Asp	Phe	Phe	Leu	Tyr	Thr	Ala	Arg	Gln	Ala	Ile	
101																220	
103	cca	gat	att	att	aat	gaa	atc	ctt	act	ttc	aaa	gtc	gac	tat	ggg	agc	720
104	Pro	Asp	Ile	Ile	Asn	Glu	Ile	Leu	Thr	Phe	Lys	Val	Asp	Tyr	Gly	Ser	
105	225															240	
107	ttc	gcc	ttt	gtt	aga	gat	aga	gct	ggt	ttt	aat	ggt	act	tca	gta	gaa	768
108	Phe	Ala	Phe	Val	Arg	Asp	Arg	Ala	Gly	Phe	Asn	Gly	Thr	Ser	Val	Glu	
109																255	
111	ggg	cag	tgc	aaa	gcc	act	cct	gga	aca	aag	att	gta	ggt	tac	tca	aca	816
112	Gly	Gln	Cys	Lys	Ala	Thr	Pro	Gly	Thr	Lys	Ile	Val	Gly	Tyr	Ser	Thr	
113																270	
115	cat	cat	gag	cat	ctc	caa	cgc	cag	agg	gtc	tca	ttt	gag	cag	gta	aaa	864
116	His	His	Glu	His	Leu	Gln	Arg	Gln	Arg	Val	Ser	Phe	Glu	Gln	Val	Lys	
117																285	
119	cgg	ata	atg	gag	ctg	cta	gag	tac	ata	gaa	gca	ctt	tat	cca	tca	ttg	912
120	Arg	Ile	Met	Glu	Leu	Leu	Glu	Tyr	Ile	Glu	Ala	Leu	Tyr	Pro	Ser	Leu	
121																300	
123	cag	gct	ttt	cag	aag	gac	tat	gaa	aaa	tat	gct	gca	aaa	gac	ttc	cag	960
124	Gln	Ala	Leu	Gln	Lys	Asp	Tyr	Glu	Lys	Tyr	Ala	Ala	Lys	Asp	Phe	Gln	
125	305															320	
127	gac	agg	gtg	cag	gca	ctc	tgt	ttt	gag	tgg	tta	aac	atc	aca	aaa	gac	1008
128	Asp	Arg	Val	Gln	Ala	Leu	Cys	Leu	Trp	Leu	Asn	Ile	Thr	Lys	Asp	Leu	
129																335	

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131	aat cag aaa tta agg att atg ggc act gtt ttg ggc atc aag aat tta	1056
132	Asn Gln Lys Leu Arg Ile Met Gly Thr Val Leu Gly Ile Lys Asn Leu	
133	340 345 350	
135	tca gac att ggc tgg cca gtg ttt gaa atc cct tcc cct cga cca tcc	1104
136	Ser Asp Ile Gly Trp Pro Val Phe Glu Ile Pro Ser Pro Arg Pro Ser	
137	355 360 365	
139	aaa ggt aat gag ccg gag tat gag ggt gat gac aca gaa gga gaa tta	1152
140	Lys Gly Asn Glu Pro Glu Tyr Glu Gly Asp Asp Thr Glu Gly Glu Leu	
141	370 375 380	
143	aag gag ttg gaa agt agt acg gat gag agt gaa gaa gaa caa atc tct	1200
144	Lys Glu Leu Glu Ser Ser Thr Asp Glu Ser Glu Glu Glu Gln Ile Ser	
145	385 390 395 400	
147	gat cct agg gta ccg gaa atc aga cag ccc ata gat aac agc ttc gac	1248
148	Asp Pro Arg Val Pro Glu Ile Arg Gln Pro Ile Asp Asn Ser Phe Asp	
149	405 410 415	
151	atc cag tcg cgg gac tgc ata tcc aag aag ctt gag agg ctc gaa tct	1296
152	Ile Gln Ser Arg Asp Cys Ile Ser Lys Lys Leu Glu Arg Leu Glu Ser	
153	420 425 430	
155	gag gat gat tct ctt ggc tgg gga gca cca gac tgg agc aca gaa gca	1344
156	Glu Asp Asp Ser Leu Gly Trp Gly Ala Pro Asp Trp Ser Thr Glu Ala	
157	435 440 445	
159	ggc ttt agt aga cat tgt ctg act tct att tat aga cca ttt gta gac	1392
160	Gly Phe Ser Arg His Cys Leu Thr Ser Ile Tyr Arg Pro Phe Val Asp	
161	450 455 460	
163	aaa gca ctg aag cag atg ggg tta aga aag tta att tta aga ctt cac	1440
164	Lys Ala Leu Lys Gln Met Gly Leu Arg Lys Leu Ile Leu Arg Leu His	
165	465 470 475 480	
167	aag cta atg gat ggt tcc ttg caa agg gca cgt ata gca ttg gta aag	1488
168	Lys Leu Met Asp Gly Ser Leu Gln Arg Ala Arg Ile Ala Leu Val Lys	
169	485 490 495	
171	aac gat cgt cca gtg gag ttt tct gaa ttt cca gat ccc atg tgg ggt	1536
172	Asn Asp Arg Pro Val Glu Phe Ser Glu Phe Pro Asp Pro Met Trp Gly	
173	500 505 510	
175	tca gat tat gtg cag ttg tca agg aca cca cct tca tct gag gag aaa	1584
176	Ser Asp Tyr Val Gln Leu Ser Arg Thr Pro Pro Ser Ser Glu Glu Lys	
177	515 520 525	
179	tgc agt gct gtg tcg tgg gag gag ctg aag gcc atg gat tta cct tca	1632
180	Cys Ser Ala Val Ser Trp Glu Glu Leu Lys Ala Met Asp Leu Pro Ser	
181	530 535 540	
183	tcc gaa cct gcc ttc cta gtt ctc tgc cga gtc ctt ctg aat gtc ata	1680
184	Phe Glu Pro Ala Phe Leu Val Leu Cys Arg Val Leu Leu Asn Val Ile	
185	545 550 555 560	
187	cat gag tgt ctg aag tta aga ttg gag cag aga cct gct gga gaa cca	1728
188	His Glu Cys Leu Lys Leu Arg Leu Glu Gln Arg Pro Ala Gly Glu Pro	
189	565 570 575	
191	tct ctc ttg agt att aag cag ctg gtg aga gag tgt aag gag gtc ctg	1776
192	Ser Leu Leu Ser Ile Lys Gln Leu Val Arg Glu Cys Lys Glu Val Leu	
193	580 585 590	
195	aag ggc ggc ctg ctg aag cag tac tac cag ttc atg ctg cag gag	1824

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196 Lys Gly Gly Leu Leu Met Lys Gln Tyr Tyr Gln Phe Met Leu Gln Glu		
197 595	600	605
199 gtt ctg gag gac ttg gag aag ccc gac tgc aac att gac gct ttt gaa		1872
200 Val Leu Glu Asp Leu Glu Lys Pro Asp Cys Asn Ile Asp Ala Phe Glu		
201 610	615	620
203 gag gat cta cat aaa atg ctt atg gtg tat ttt gat tac atg aga agc		1920
204 Glu Asp Leu His Lys Met Leu Met Val Tyr Phe Asp Tyr Met Arg Ser		
205 625	630	635
207 tgg atc caa atg cta cag caa tta cct caa gca tcg cat agt tta aaa		1968
208 Trp Ile Gln Met Leu Gln Gln Leu Pro Gln Ala Ser His Ser Leu Lys		
209 645	650	655
211 aat ctg tta gaa gaa gaa tgg aat ttc acc aaa gaa ata act cat tac		2016
212 Asn Leu Leu Glu Glu Trp Asn Phe Thr Lys Glu Ile Thr His Tyr		
213 660	665	670
215 ata cgg gga gga gaa gca cag gcc ggg aag ctt ttc tgt gac att gca		2064
216 Ile Arg Gly Gly Glu Ala Gln Ala Gly Lys Leu Phe Cys Asp Ile Ala		
217 675	680	685
219 gga atg ctg ctg aaa tct aca gga agt ttt tta gaa ttt ggc tta cag		2112
220 Gly Met Leu Leu Lys Ser Thr Gly Ser Phe Leu Glu Phe Gly Leu Gln		
221 690	695	700
223 gag agc tgt gct gaa ttt tgg act agt gcg gat gac agc agt gct tcc		2160
224 Glu Ser Cys Ala Glu Phe Trp Thr Ser Ala Asp Asp Ser Ser Ala Ser		
225 705	710	715
227 gac gaa atc agg agg tct gtt ata gag atc agt cga gcc ctg aag gag		2208
228 Asp Glu Ile Arg Arg Ser Val Ile Glu Ile Ser Arg Ala Leu Lys Glu		
229 725	730	735
231 ctc ttc cat gaa gcc aga gaa agg gct tcc aaa gca ctt gga ttt gct		2256
232 Leu Phe His Glu Ala Arg Glu Arg Ala Ser Lys Ala Leu Gly Phe Ala		
233 740	745	750
235 aaa atg ttg aga aag gac ctg gaa ata gca gca gaa ttc agg ctt tca		2304
236 Lys Met Leu Arg Lys Asp Leu Glu Ile Ala Ala Glu Phe Arg Leu Ser		
237 755	760	765
239 gcc cca gtt aga gac ctc ctg gat gtt ctg aaa tca aaa cag tat gtc		2352
240 Ala Pro Val Arg Asp Leu Leu Asp Val Leu Lys Ser Lys Gln Tyr Val		
241 770	775	780
243 aag gtg caa att cct ggg tta gaa aac ttg caa atg ttt gtt cca gac		2400
244 Lys Val Gln Ile Pro Gly Leu Glu Asn Leu Gln Met Phe Val Pro Asp		
245 785	790	795
247 act ctt gct gag gag aag agt att att ttg cag tta ctc aat gca gct		2448
248 Thr Leu Ala Glu Glu Lys Ser Ile Ile Leu Gln Leu Leu Asn Ala Ala		
249 805	810	815
251 gca gga aag gac tgt tca aaa gat tca gat gac gta ctc atc gat gcc		2496
252 Ala Gly Lys Asp Cys Ser Lys Asp Ser Asp Asp Val Leu Ile Asp Ala		
253 820	825	830
255 tat ctg ctt ctg acc aag cac ggt gat cga gcc cgt gat tca gag gac		2544
256 Tyr Leu Leu Leu Thr Lys His Gly Asp Arg Ala Arg Asp Ser Glu Asp		
257 835	840	845
259 agc tgg ggc acc tgg gag gca cag cct gtc aaa gtc gtg cct cag gtg		2592
260 Ser Trp Gly Thr Trp Glu Ala Gln Pro Val Lys Val Val Pro Gln Val		

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261	850	855	860	
263	gag act gtt gac acc ctg aga agc atg cag gtg gat aat ctt tta cta			2640
264	Glu Thr Val Asp Thr Leu Arg Ser Met Gln Val Asp Asn Leu Leu Leu			
265	865	870	875	880
267	gtt gtc atg cag tct gcg cat ctc aca att cag aga aaa gct ttc cag			2688
268	Val Val Met Gln Ser Ala His Leu Thr Ile Gln Arg Lys Ala Phe Gln			
269	885	890	895	
271	cag tcc att gag gga ctt atg act ctg tgc cag gag cag aca tcc agt			2736
272	Gln Ser Ile Glu Gly Leu Met Thr Leu Cys Gln Glu Gln Thr Ser Ser			
273	900	905	910	
275	cag ccg gtc atc gcc aaa gct ttg cag cag ctg aag aat gat gca ttg			2784
276	Gln Pro Val Ile Ala Lys Ala Leu Gln Gln Leu Lys Asn Asp Ala Leu			
277	915	920	925	
279	gag cta tgc aac agg ata agc aat gcc att gac cgc gtg gac cac atg			2832
280	Glu Leu Cys Asn Arg Ile Ser Asn Ala Ile Asp Arg Val Asp His Met			
281	930	935	940	
283	tcc aca tca gaa ttt gat gct gag gtt gat gaa tct gaa tct gtc acc			2880
284	Phe Thr Ser Glu Phe Asp Ala Glu Val Asp Glu Ser Glu Ser Val Thr			
285	945	950	955	960
287	ttg caa cag tac tac cga gaa gca atg att cag ggg tac aat ttt gga			2928
288	Leu Gln Gin Tyr Tyr Arg Glu Ala Met Ile Gln Gly Tyr Asn Phe Gly			
289	965	970	975	
291	ttt gag tat cat aaa gaa gtt gtt cgt ttg atg tct ggg gag ttt aga			2976
292	Phe Glu Tyr His Lys Glu Val Val Arg Leu Met Ser Gly Glu Phe Arg			
293	980	985	990	
295	cag aag ata gga gac aaa tat ata agc ttt gcc cgg aag tgg atg aat			3024
296	Gln Lys Ile Gly Asp Lys Tyr Ile Ser Phe Ala Arg Lys Trp Met Asn			
297	995	1000	1005	
299	tat gtc ctg act aaa tgt gag agt ggt aga ggt aca aga ccc agg tgg			3072
300	Tyr Val Leu Thr Lys Cys Glu Ser Gly Arg Gly Thr Arg Pro Arg Trp			
301	1010	1015	1020	
303	gct act caa gga ttt gat ttt cta caa gca att gaa cct gcc ttt att			3120
304	Ala Thr Gln Gly Phe Asp Phe Leu Gln Ala Ile Glu Pro Ala Phe Ile			
305	1025	1030	1035	1040
307	tca gct tta cca gaa gat gac ttc ttg agt tta caa gcc ttg atg aat			3168
308	Ser Ala Leu Pro Glu Asp Asp Phe Leu Ser Leu Gln Ala Leu Met Asn			
309	1045	1050	1055	
311	gaa tgc att ggc cat gtc ata gga aaa cca cac agt cct gtt aca ggt			3216
312	Glu Cys Ile Gly His Val Ile Gly Lys Pro His Ser Pro Val Thr Gly			
313	1060	1065	1070	
315	ttg tac ctt gcc att cat cgg aac agc ccc cgt cct atg aag gta cct			3264
316	Leu Tyr Leu Ala Ile His Arg Asn Ser Pro Arg Pro Met Lys Val Pro			
317	1075	1080	1085	
319	cga tgc cat agt gac cct cct aac cca cac ctc att atc ccc act cca			3312
320	Arg Cys His Ser Asp Pro Pro Asn Pro His Leu Ile Ile Pro Thr Pro			
321	1090	1095	1100	
323	gag gga ttc agg ggt tcc agc gtt cct gaa aat gat cga ttg gct tcc			3360
324	Glu Gly Phe Arg Gly Ser Ser Val Pro Glu Asn Asp Arg Leu Ala Ser			
325	1105	1110	1115	1120

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:31 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:420 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:445 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:456 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:1389 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:1411 M:258 W: Mandatory Feature missing, <220> FEATURE: